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RAW SEQUENCE LISTING

DATE: 04/26/2001

PATENT APPLICATION: US/09/766,778

TIME: 10:42:08

Input Set : N:\Crf3\RULE60\09766778.txt

Output Set: N:\CRF3\04262001\1766778.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Papathanassiou, Adonia E
 7 Green, Shawn J.

9 (ii) TITLE OF INVENTION: Compositions and Methods for Inhibiting
 10 Cellular Proliferation

12 (iii) NUMBER OF SEQUENCES: 2

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Jones & Askew
 16 (B) STREET: 191 Peachtree Street, 37th Floor
 17 (C) CITY: Atlanta
 18 (D) STATE: Georgia
 19 (E) COUNTRY: U.S.A.
 20 (F) ZIP: 30303

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk
 24 (B) COMPUTER: IBM PC compatible
 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/766,778

C--> 30 (B) FILING DATE: 22-Jan-2001

31 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 09/227,955
 35 (B) FILING DATE:

37 (viii) ATTORNEY/AGENT INFORMATION:

38 (A) NAME: Greene, Jamie L.
 39 (B) REGISTRATION NUMBER: 32,467
 40 (C) REFERENCE/DOCKET NUMBER: 05213-0290

42 (ix) TELECOMMUNICATION INFORMATION:

43 (A) TELEPHONE: (404) 818-3700
 44 (B) TELEFAX: (404) 818-3799

47 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 276 amino acids
 51 (B) TYPE: amino acid
 52 (C) STRANDEDNESS: single
 53 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

57 (iii) HYPOTHETICAL: NO

59 (iv) ANTI-SENSE: NO

61 (v) FRAGMENT TYPE: N-terminal

63 (vi) ORIGINAL SOURCE:

64 (A) ORGANISM: Homo sapiens

66 (ix) FEATURE:

67 (A) NAME/KEY: Active Site

ENTERED

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68         (B) LOCATION: 2..3
69         (D) OTHER INFORMATION: /note= "Site of partial
70 phosphorylation."
71         (ix) FEATURE:
72         (A) NAME/KEY: Active site
73         (B) LOCATION: 117..118
74         (D) OTHER INFORMATION: /note= "Potential site for N-linked
75 glycosylation"
76         (ix) FEATURE:
77         (A) NAME/KEY: Active-site
78         (B) LOCATION: 167..168
79         (D) OTHER INFORMATION: /note= "Potential site for N-linked
80 glycosylation"
81         (ix) FEATURE:
82         (A) NAME/KEY: Active-site
83         (B) LOCATION: 223..229
84         (D) OTHER INFORMATION: /note= "Potential site for N-linked
85 glycosylation"
86         (ix) FEATURE:
87         (A) NAME/KEY: Domain
88         (B) LOCATION: 26..76
89         (D) OTHER INFORMATION: /label= Kunitz-1
90         (ix) FEATURE:
91         (A) NAME/KEY: Domain
92         (B) LOCATION: 97..147
93         (D) OTHER INFORMATION: /label= Kunitz-2
94         (ix) FEATURE:
95         (A) NAME/KEY: Domain
96         (B) LOCATION: 189..239
97         (D) OTHER INFORMATION: /label= Kunitz-3
98         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1
99         Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu
100         1          5          10          15
101         Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp
102         20          25          30
103         Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr
104         35          40          45
105         Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn
106         50          55          60
107         Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn
108         65          70          75          80
109         Ala Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe
110         85          90          95
111         Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg
112         100         105         110
113         Tyr Phe Thr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly
114         115         120         125
115         Gly Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys
116         130         135         140

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135 Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly
136 145 150 155 160
138 Thr Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys
139 165 170 175
141 Val Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro
142 180 185 190
144 Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn
145 195 200 205
147 Ser Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly
148 210 215 220
150 Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys
151 225 230 235 240
153 Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys
154 245 250 255
156 Arg Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe
157 260 265 270
159 Val Lys Asn Met
160 275

```

162 (2) INFORMATION FOR SEQ ID NO: 2:

164 (i) SEQUENCE CHARACTERISTICS:

165 (A) LENGTH: 213 amino acids

166 (B) TYPE: amino acid

167 (C) STRANDEDNESS: single

168 (D) TOPOLOGY: linear

170 (ii) MOLECULE TYPE: protein

172 (iii) HYPOTHETICAL: NO

174 (iv) ANTI-SENSE: NO

176 (v) FRAGMENT TYPE: N-terminal

178 (vi) ORIGINAL SOURCE:

179 (A) ORGANISM: Homo sapiens

183 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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185 Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn Ala Glu Ile Cys Leu Leu
186 1 5 10 15
188 Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu Leu Leu Arg Tyr Tyr
189 20 25 30
191 Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe Leu Tyr Gly Gly Cys Glu
192 35 40 45
194 Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu Ala Cys Asp Asp Ala Cys
195 50 55 60
197 Trp Arg Ile Glu Lys Val Pro Lys Val Cys Arg Leu Gln Val Ser Val
198 65 70 75 80
200 Asp Asn Gln Cys Glu Gly Ser Ile Gln Lys Tyr Phe Phe Asn Leu Ser
201 85 90 95
203 Ser Met Thr Cys Gln Lys Phe Phe Ser Gly Gly Cys His Arg Asn Arg
204 100 105 110
206 Ile Ile Asn Arg Phe Pro Asp Glu Ala Thr Cys Met Gly Phe Cys Ala
207 115 120 125
209 Pro Lys Lys Ile Pro Ser Phe Cys Tyr Ser Pro Lys Asp Glu Gly Leu
210 130 135 140

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212	Cys Ser Ala Asn Val Thr Arg Tyr Tyr Phe Asn Pro Arg Tyr Arg Thr
213	145 150 155 160
215	Cys Asp Ala Phe Thr Tyr Thr Gly Cys Gly Gly Asn Asp Asn Asn Phe
216	165 170 175
218	Val Ser Arg Glu Asp Cys Lys Arg Ala Cys Ala Lys Ala Leu Lys Lys
219	180 185 190
221	Lys Lys Lys Met Pro Lys Leu Arg Phe Ala Ser Arg Ile Arg Lys Ile
222	195 200 205
224	Arg Lys Lys Gln Phe
225	210

VERIFICATION SUMMARY

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]